What is Claimed is:

1. An isolated polynucleotide comprising or consisting of a nucleic acid sequence selected from the group consisting of:

(a) SEQ ID NO: 1 or 3;

(b) a nucleic acid sequence that is a degenerate variant of SEQ ID NO: 1 or 3;

(c) a nucleic acid sequence at least 78% identical to SEQ ID NO: 1 or 3;

(d) a nucleic acid sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO:2 or 4;

(e) a nucleic acid sequence that encodes a polypeptide at least 77% identical to SEQ ID NO:2 or 4;

(f) a nucleic acid sequence that hybridizes under stringent conditions to SEQ ID NO:1 or 3; and

(g) a nucleic acid sequence comprising a fragment of any one of (a) – (f) that is at least 60 contiguous nucleotides in length.

2. An isolated polynucleotide comprising or consisting of a nucleic acid sequence selected from the group consisting of:

(a) SEQ ID NO: 1 or 3;

(b) a nucleic acid sequence that is a degenerate variant of SEQ ID NO: 1 or 3;

(c) a nucleic acid sequence at least 87% identical to SEQ ID NO: 1 or 3;

(d) a nucleic acid sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO: 2 or 4;

(e) a nucleic acid sequence that encodes a polypeptide at least 83% identical to SEQ ID NO: 2 or 4;

(f) a nucleic acid sequence that hybridizes under stringent conditions to SEQ ID NO: 1 or 3; and

(g) a nucleic acid sequence comprising a fragment of any one of (a) – (f) that is at least 60 contiguous nucleotides in length.

3. The polynucleotide of claims 1 or 2, wherein the nucleic acid sequence encodes an endomannosidase activity.

4. The polynucleotide of claims 1 or 2, wherein the nucleic acid sequence encodes a catalytically active fragment of an endomannosidase.

5. The encoded polynucleotide of claim 4 wherein the encoded endomannosidase has optimal activity at a pH between about 5.2 and about 7.2.

6. The encoded polynucleotide of claims 4 wherein the encoded endomannosidase activity has optimal activity at a pH of about pH6.2.

7. The encoded polynucleotide of claims 1 or 2 wherein the polypeptide hydrolyzes a composition comprising at least one glucose residue and one mannose residue on glucosylated glycans.

8. The encoded polynucleotide of claims 1 or 2 wherein the polypeptide hydrolyzes a Glcα1,3Man dimer, Glc$_2\alpha$1,3Man trimer or Glc$_3\alpha$1,3Man tetramer on an oligosaccharide.

9. The encoded polynucleotide of claims 1 or 2 wherein the polypeptide hydrolyzes at least one glucose residue and one mannose residue on a $Glc_{1-3}Man_5GlcNAc_2$, $Glc_{1-3}Man_6GlcNAc_2$, $Glc_{1-3}Man_7GlcNAc_2$, $Glc_{1-3}Man_8GlcNAc_2$, $Glc_{1-3}Man_9GlcNAc_2$ or glucosylated higher mannan glycans.

10. A vector comprising the polynucleotide of claims 1 or 2.

11. A fusion protein comprising the encoded polypeptide of claims 1 or 2.

12. The fusion protein of claim 11 wherein the encoded polypeptide produces a modified glycoform on a protein of interest.

13. The fusion protein of claim 11 wherein the encoded polypeptide hydrolyzes Glcα1,3Man, Glc$_2\alpha$1,3Man or Glc$_3\alpha$1,3Man.

14. A host cell comprising the polynucleotide of claims 1 or 2.

15. The host cell of claim 14 wherein the host cell is a mammalian, plant, insect, fungal, yeast, algal or bacterial cell.

16. The host cell of claim 14, wherein the host cell is selected from the group consisting of *Pichia pastoris*, *Pichia finlandica*, *Pichia trehalophila*, *Pichia koclamae*, *Pichia membranaefaciens*, *Pichia opuntiae*, *Pichia thermotolerans*, *Pichia salictaria*, *Pichia guercuum*, *Pichia pijperi*, *Pichia stiptis*, *Pichia methanolica*, *Pichia* sp., *Saccharomyces cerevisiae*, *Saccharomyces* sp., *Hansenula polymorpha*, *Kluyveromyces* sp., *Kluyveromyces lactis*, *Candida albicans*, *Aspergillus nidulans*, *Aspergillus niger, Aspergillus oryzae, Trichoderma reesei, Chrysosporium lucknowense*, *Fusarium* sp., *Fusarium gramineum, Fusarium venenatum* and *Neurospora crassa.*

17. A method for modifying glycosylation structures in a lower eukaryote comprising: expressing an endomannosidase activity wherein the endomannosidase activity removes a composition comprising at least a glucose residue and one mannose residue on an oligosaccharide.

18. The method of claim 17 wherein the endomannosidase activity further comprises the activity of truncating $Glc_{1-3}Man_{9-5}GlcNAc_2$ to $Man_{8-4}GlcNAc_2$ wherein Glcα1,3Man, $Glc_2\alpha$1,3Man or $Glc_3\alpha$1,3Man are removed.

19. The method of claim 17 wherein the endomannosidase activity comprises hydrolysis of a composition comprising at least one glucose residue and one mannose residue on glucosylated glycans.

20. The method of claim 17 wherein the endomannosidase introduced are targeted to the endoplasmic reticulum, the early, medial, late Golgi, trans Golgi network or any vesicular compartment within the host organism.

21. The method of claim 17 wherein the endomannosidase is of host origin but has been modified by mutation, promoter strength or copy number to enhance activity.

22. The method of claim 17 wherein the endomannosidase is secreted.

23. The method of claim 17 wherein the host cell is a mammalian, plant, insect, fungal, yeast, algal or bacterial cell.

24. The method of claim 17 wherein the lower eukaryote is selected from the group consisting of *Pichia pastoris*, *Pichia finlandica*, *Pichia trehalophila*, *Pichia koclamae*, *Pichia membranaefaciens*, *Pichia opuntiae*, *Pichia thermotolerans*, *Pichia salictaria*, *Pichia guercuum*, *Pichia pijperi*, *Pichia stiptis*, *Pichia methanolica*, *Pichia* sp., *Saccharomyces cerevisiae*, *Saccharomyces* sp., *Hansenula polymorpha*, *Kluyveromyces* sp., *Kluyveromyces lactis*, *Candida albicans*, *Aspergillus nidulans*, *Aspergillus niger, Aspergillus oryzae, Trichoderma reesei, Chrysosporium lucknowense*, *Fusarium* sp., *Fusarium gramineum, Fusarium venenatum* and *Neurospora crassa.*

25. A method for modifing glucosylated glycoproteins comprising introducing an endomannosidase activity in a lower eukaryotic host cell wherein upon expression of the endomannosidase activity modifies a glucosylated glycoprotein that has bypassed the ER.